

Appl. No. 09/851,058

Amendment dated July 1, 2004

Reply to Office Action of March 10, 2004

Please amend the application as follows:

Amendments to the Specification:

Please replace the Abstract with the following:

ABSTRACT

Methods using gel electrophoresis and mass spectrometry for the rapid, quantitative analysis of proteins or protein function in mixtures of proteins derived from two or more samples in one unit operation are disclosed. In one embodiment the method includes (a) preparing an extract of proteins from each of at least two different samples; (b) providing a set of substantially chemically two or more structurally identical and differentially isotopically labeled protein reagents, one set for each sample; (c) reacting the extract each set of proteins from different samples of step (a) with a different isotopically labeled reagent from the set of step (b) to provide two or more sets of isotopically, but differentially labeled proteins; (d) mixing each of the two or more sets of isotopically labeled proteins to form a single mixture of different isotopically differentially labeled proteins; (e) electrophoresing the mixture of step (d) by an electrophoresing method capable of separating proteins within the mixture; (f) digesting at least a portion of one or more separated proteins of step (e) and (f)(g) detecting the difference in the expression levels of the proteins in the two samples by mass spectrometry based on individual one or more peptides in the sample of labeled peptides derived from chemical or enzymatic digestion. The analytical method can be used for qualitative and particularly for quantitative analysis of global protein expression profiles in cells and tissues, i.e. the quantitative analysis of proteomes.